

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 27, 2001, 16:43:09 ; Search time 38.23 Seconds
(without alignments)
1128.209 Million cell updates/sec

Title: US-09-483-543a-9
Perfect score: 1733
Sequence: 1 KRGCAGNDFSEERSWTWGR.....SGCGXGLEVLFGQVRRKXG 326

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL_16:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------------|
| 1 | 1078 | 62.2 | 239 | 11 | Q9QW60 mus sp. grb |
| 2 | 834.5 | 48.2 | 255 | 14 | Q99059 avian sarco |
| 3 | 343 | 19.8 | 279 | 5 | Q9NHC3 Q9nnc3 caenorhabdi |
| 4 | 213 | 12.3 | 217 | 13 | Q9PU11 Q9pu11 xenopus lae |
| 5 | 200 | 11.5 | 600 | 5 | Q9VE96 Q9ve96 drosophila |
| 6 | 193 | 11.1 | 1067 | 13 | Q9YHU6 Q9yhu6 xenopus lae |
| 7 | 184.5 | 10.6 | 1010 | 13 | Q9YHU7 Q9yhu7 xenopus lae |
| 8 | 182 | 10.5 | 1097 | 5 | Q9U2T9 Q9u2t9 caenorhabdi |
| 9 | 173 | 10.0 | 640 | 4 | Q60593 Q60593 homo sapien |
| 10 | 170 | 9.8 | 816 | 4 | Q60592 Q60592 homo sapien |
| 11 | 165 | 9.5 | 1270 | 13 | Q42287 Q42287 xenopus lae |
| 12 | 164 | 9.5 | 1196 | 11 | Q35413 Q35413 rattus norv |
| 13 | 163.5 | 9.4 | 857 | 3 | Q9P7E8 Q9p7e8 schizosacch |
| 14 | 163 | 9.4 | 684 | 4 | Q9Y338 Q9y338 homo sapien |
| 15 | 162 | 9.3 | 815 | 4 | Q9P200 Q9p2q0 homo sapien |
| 16 | 162 | 9.3 | 1217 | 11 | Q9WVE9 Q9wve9 rattus norv |
| 17 | 161 | 9.3 | 1094 | 5 | Q61618 Q61618 drosophila |
| 18 | 161 | 9.3 | 1097 | 5 | Q9V1F7 Q9v1f7 drosophila |

| | | | | | | |
|----|-------|-----|------|----|--------|---------------------|
| 20 | 161 | 9.3 | 1100 | 4 | Q94875 | Q94875 homo sapien |
| 21 | 160 | 9.2 | 1721 | 4 | Q95216 | Q95216 homo sapien |
| 22 | 159 | 9.2 | 1220 | 4 | Q9UET5 | Q9uets5 homo sapien |
| 23 | 159 | 9.2 | 1721 | 4 | Q9UNK2 | Q9unk2 homo sapien |
| 24 | 158 | 9.1 | 1004 | 4 | Q9UHN7 | Q9uhn7 homo sapien |
| 25 | 158 | 9.1 | 1220 | 4 | Q9UNK1 | Q9unk1 homo sapien |
| 26 | 157.5 | 9.1 | 820 | 11 | Q9QZK2 | Q9qzk2 mus musculu |
| 27 | 157 | 9.1 | 1248 | 4 | Q9NZM2 | Q9nzm2 mus sapien |
| 28 | 157 | 9.1 | 1676 | 4 | Q9ULG4 | Q9ulg4 homo sapien |
| 29 | 157 | 9.1 | 1681 | 4 | Q9NYG0 | Q9nyg0 homo sapien |
| 30 | 157 | 9.1 | 1696 | 4 | Q9NZM3 | Q9nzm3 homo sapien |
| 31 | 156.5 | 9.0 | 330 | 4 | Q9NRU7 | Q9nru7 homo sapien |
| 32 | 156.5 | 9.0 | 500 | 5 | Q9V5J3 | Q9v5j3 drosophila |
| 33 | 156 | 9.0 | 939 | 5 | Q24145 | Q24145 drosophila |
| 34 | 155 | 8.9 | 505 | 5 | Q97337 | Q97337 paracentrot |
| 35 | 154.5 | 8.9 | 684 | 11 | Q62417 | Q62417 mus musculu |
| 36 | 154.5 | 8.9 | 714 | 11 | Q9Z0Z8 | Q9z0z8 mus musculu |
| 37 | 154.5 | 8.9 | 724 | 11 | Q9Z0Z9 | Q9z0z9 mus musculu |
| 38 | 154 | 8.9 | 825 | 4 | Q75815 | Q75815 mus sapien |
| 39 | 153 | 8.8 | 1714 | 11 | Q9Z0R4 | Q9z0r4 mus sapien |
| 40 | 152.5 | 8.8 | 1011 | 5 | Q61639 | Q61639 drosophila |
| 41 | 152 | 8.8 | 954 | 5 | Q97180 | Q97180 drosophila |
| 42 | 151.5 | 8.7 | 334 | 5 | Q9PYR3 | Q9pyr3 caenorhabdi |
| 43 | 151 | 8.7 | 1146 | 11 | Q9WVE1 | Q9wve1 rattus norv |
| 44 | 151 | 8.7 | 1186 | 5 | Q61080 | Q61080 acanthamoeb |
| 45 | 150.5 | 8.7 | 687 | 11 | Q9QY53 | Q9qy53 mus musculu |

ALIGNMENTS

RESULT 1
Q9QW60 PRELIMINARY; PRT; 239 AA.
ID Q9QW60:
AC Q9QW60:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GRB-3-EPIDERMAL GROWTH FACTOR-RECEPTOR-BINDING PROTEIN.
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93028373; PubMed=1409582;
RA Marcolis B., Silvenoinen O., Comoglio F., Roonprapant C., Skolnik E.,
RA Ullrich A., Schlessinger J.;
RT "High-efficiency expression/cloning of epidermal growth factor-
RT receptor-binding proteins with Src homology 2 domains.";
RT Proc. Natl. Acad. Sci. U.S.A. 89:8894-8898(1992).
DR HSP; Q64010; ICKA.
DR Interpro: IPR000980;
DR Interpro: IPR001452;
DR Interpro: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
DR SMART; SM00326; SH3; 1.
SQ SEQUENCE 239 AA; 26013 MW; 48326D680CF09B6 CRC64;

Query Match

Best Local Similarity 62.2%; Score 1078; DB 11; Length 239;
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGNPFSEERSMYWGRSLRQEAVALLOGRHGFLVRDSTSPGQYVLVSSENSRVSHYI 64
|||||
DB 33 AGNPFSEERSMYWGRSLRQEAVALLOGRDGCVFLVRDSTSPGQYVLVSSENSRVSHYI 92
QY 65 INSSGPRPPVPPSPAPQPPGVSFSLRLRIGDQFDSLPALEFYKIHVDTTLLIEPVARS 124

DB 93 INSSGRPPVPPSPAPPPGSPSRLRIGDQEDSLPALLEFYKHYLDITTLIEPVARS 152
QY 125 RQSGSVILRQEAEEYVRALEFDNGNDEEDLPFKKGDIIRDRKPEEOMWNAEDSEGRKM 184
DB 153 RQSGSVILRQEAEEYVRALEFDNGNDEEDLPFKKGDIIRDRKPEEOMWNAEDSEGRKM 212
QY 185 IPPPYEYKTRPASASVSALIGNOBSS 211
DB 213 IPPVYKTRPASASVSALIGNOBSS 239

RESULT 2

099059 PRELIMINARY; PRT; 255 AA.
AC 099059;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE GAG-CRK PROTEIN (FRAGMENT).
OS Avian sarcoma virus 1.
OC Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
OX NCBI_Taxid=11957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90045469; PubMed=2554234;
RA Tsuchie H., Chang C.H.W., Yoshida M., Vogt P.K.;
RT "A newly isolated avian sarcoma virus, ASV-1, carries the crk oncogene.";
RT Oncogene 4:1281-1284(1989).
CC -1- SIMILARITY: CONTAINS A COPY EACH OF THE SH2 AND SH3 DOMAINS.
DR EMBL: X17292; CA35181.1; -.
DR HSP: 064010; 1CRK.
DR InterPro: IPR000980; -.
DR InterPro: IPR001452; -.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
DR SMART: SM00326; SH3; 1.
KW Oncogene; Polyprotein; SH3 domain; SH2 domain.
FT NON_TER 1
FT DOMAIN <1 23 GAG (BY SIMILARITY).
FT DOMAIN 24 253 CRK (BY SIMILARITY).
FT DOMAIN 63 112 SH2 (OR B+C BOX) (BY SIMILARITY).
FT DOMAIN 188 239 SH3 (OR A BOX) (BY SIMILARITY).
FT DOMAIN 254 255 GAG (BY SIMILARITY).
SQ SEQUENCE 255 AA; 27985 MW; 0C562D0B2327A579 CRC64;

Query Match 48.2%; Score 834.5; DB 14; Length 255;
Best Local Similarity 78.3%; Pred. No. 2.5e-61;
Matches 159; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

QY 5 AGFDESEERSSMWGRSLRQEAVALLOGRHGVFLVRSSTPGDYVLSVSNRSRSHYI 64
DB 52 AGGFDESEERSSMWGRSLRQEAVALLOGRHGVFLVRSSTPGDYVLSVSNRSRSHYI 111
QY 65 INSSGRPPVPPSPAP-PPGVSPSRLRIGDQEDSLPALLEFYKHYLDITTLIEPVAR 123
DB 112 VNSLGRAGRRRAGGEGPAGPGLNPTFRIGDQEDSLPALLEFYKHYLDITTLIEPVAR 171
QY 124 SROGSGVILRQEAEEYVRALEFDNGNDEEDLPFKKGDIIRDRKPEEOMWNAEDSEGRKM 183
DB 172 SROGSGVILRQEAEEYVRALEFDNGNDEEDLPFKKGDIIRDRKPEEOMWNAEDSEGRKM 231
QY 184 MIPVYKTRPASASVSALIG 206
DB 232 MIPVYKTRPASASVSALIG 254

RESULT 3
09NHC3 PRELIMINARY; PRT; 279 AA.
AC 09NHC3;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE CELL-CORPSE ENGULFMENT PROTEIN CED-2.
GN CED-2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Reddien P.W., Horvitz H.R.;
RT "CED-2/CrkII and CED-10/Rac control phagocytosis and cell migration in C. elegans.";
RT Nat. Cell Biol. 0:0-0(2000).
RL EMBL: AF226866; AF33845.1; -.
DR InterPro: IPR000980; -.
DR InterPro: IPR001452; -.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 2.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
SQ SEQUENCE 279 AA; 30878 MW; 5CE7DA478948970B CRC64;

Query Match 19.8%; Score 343; DB 5; Length 279;
Best Local Similarity 31.0%; Pred. No. 1.2e-20;
Matches 93; Conservative 52; Mismatches 111; Indels 44; Gaps 9;

QY 8 FDSEERSSMWGRSLRQEAVALLOGRHGVFLVRSSTPGDYVLSV---SENSRVS 61
DB 6 FDPFEMRSEFYFGMSRREAHKLL-GEPPVSGTGLMDS--RPEYSUTVREADEGNAYC 63
QY 62 HYIINSGRPPVPPSPAPPPGSPSRLRIGDQEDSLPALLEFYKHYLDITTLIEPV 121
DB 64 HYLIERGEPR-----EDGTAAGVKTANOSFPDIPALNHFMRVLTASLL-- 110
QY 122 ARSROGSGVILRQEAEEYVRALEFDNGNDEEDLPFKKGDIIRDRKPEEOMWNAEDSEK 181
DB 111 -----AAKKPLIEVVGTFKFTGERETDLPEFGGERELISKTINQDMWRNALGT 162
QY 182 RGMIPVPEVE--KYRPASASVSALIGNOGESHPPQIGPEPGPYAQPVSNTPLNLQ- 237
DB 183 TGLVPANYVQLOMERHNDRTS-----KGASQSSIGSGGGAERFSSASTSDNIEL 213
QY 238 --NGPITARYQKVPNAYDKTALALEVGLYKTKINVSQMGSEONCKRGHPRFTNVR 295
DB 214 QRLPEAKAKVTFDRVPNAVYDPTLRVKKGTVLVTQKMSNGMYAEILDQIGSVPHYLR 273
RESULT 4
09P011 PRELIMINARY; PRT; 217 AA.
AC 09P011;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE GRB2 PROTEIN.
GN GRB2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Goisset C., Shi D.L., Boucaut J.C.;

| RESULT | 5 | |
|--------|---|---------------------------|
| 09VE96 | | |
| ID | 09VE96 | PRELIMINARY; PRT; 600 AA. |
| AC | 09VE96; | |
| DT | 01-MAY-2000 (TREMBLrel. 13, Created) | |
| DT | 01-MAY-2000 (TREMBLrel. 13, last sequence update) | |
| DT | 01-MAR-2001 (TREMBLrel. 16, last annotation update) | |
| DE | CG1129 PROTEIN. | |
| GN | CG1129. | |
| OS | Drosophila melanogaster (Fruit fly). | |
| OC | Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; | |
| OC | Pterygota; Neoptera; Endopterygota; Diptera; Muscomorpha; | |
| OC | Ephydroidea; Drosophilidae; Drosophila. | |
| OX | NCBI_TaxId=7227; | |
| RP | [1] | |
| RC | SEQUENCE FROM N.A. | |
| RC | STRAIN=BERKELEY; | |
| RX | MEDLINE=20196006; PubMed=10731132; | |
| RA | Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., | |
| RA | Amantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., | |
| RA | George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., | |
| RA | Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., | |
| RA | Brandon R.C., Rogers Y.H.C., Blazy R.G., Champe M., Pfeiffer B.D., | |
| RA | Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., | |
| RA | Adair J.F., Agayanni A., An H.-J., Andrews-Pfannkoch C., Baldwin D., | |
| RA | Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., | |
| RA | Beeson K.Y., Beos P.V., Berman B.P., Bhandari D., Bolshakov S., | |
| RA | Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P., | |
| RA | Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., | |
| RA | Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies J., | |
| RA | de Pallos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., | |
| RA | Dodon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., | |
| RA | Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., | |

| | | |
|--------|---|---------------|
| RESULT | 6 | |
| Q9YHU6 | | |
| Q9YHU6 | PRELIMINARY; | PRT: 1067 AA. |
| AC | Q9YHU6; | |
| DT | 01-MAY-1999 (TREMBREL, 10, Created) | |
| DT | 01-MAY-1999 (TREMBREL, 10, last sequence update) | |
| DT | 01-MAR-2001 (TREMBREL, 16, last annotation update) | |
| DE | PHOSPHOLIPASE C-GAMMA-1b (FRAGMENT). | |
| OS | Xenopus laevis (African clawed frog). | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| OC | Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae; | |
| CC | Xenopodidae; Xenopus. | |

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OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kung H.-F., Kim J., Huang Y.K., Lin M.C.;
RT "Molecular cloning of two different forms of Xenopus phospholipase C-
gamma-1."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF090112; AAD03595.1; -.
DR HSSP; P08487; 2PLD.
DR InterPro; IPR000008; -.
DR InterPro; IPR000909; -.
DR InterPro; IPR000980; -.
DR InterPro; IPR001192; -.
DR InterPro; IPR001452; -.
DR InterPro; IPR001711; -.
DR InterPro; IPR001849; -.
DR InterPro; IPR002048; -.
DR Pfam; PF000017; SH2; 2.
DR Pfam; PF000018; SH3; 1.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00169; PH; 2.
DR Pfam; PF00387; PI-PLC-Y; 1.
DR Pfam; PF00388; PI-PLC-X; 1.
DR PRINTS; PR00390; PHPLIPASEC.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PH_DOMAIN; 1.
DR PROSITE; PS50003; PI-PLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50001; SH2; 2.
DR PROSITE; PS50002; SH3; 1.
DR SMART; SM00239; C2; 1.
FT NON_TER 1
FT NON_TER 1067
SQ SEQUENCE 1067 AA; 124019 MW; 533F6876ECDFE5DB CRC64;

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Query Match      11.1%; Score 193; DB 13; Length 1067;
Best Local Similarity 21.7%; Pred. No. 1.8e-07;
Matches 95; Conservative 43; Mismatches 123; Indels 176; Gaps 17;

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OY 3 GCAGNFDESER-----SSWYWGRL-----SRQEAVALL-----OGQRHGVL 39
DB 396 GSOANDDEEOKASNSSELSAEMKWFHGLGAGRDGRHIAERLLTDYCIETGADGGSFL 455
OY 40 VRDSTSPGQVYLSVSENSRSHYIINS-----SGPR-----KIHYDITTLIEPV 71
DB 456 VRSETFVGDTYLSFWKNGKVQHCRIHSROEAGSPKLLTDNLVESLYALTLTHQOMPL 515
OY 72 -----PPVPSPAQ-----PPGVSPSRLR----- 91
DB 516 RCNEFEMRLTEPVQTNHAESKEWYHASLTRQAEHMLKRVPRDGAFLVRRKSEQNSYAI 575
OY 92 -----IGDQFDSLPALLEY-----KIHYDITTLIEPV 121
DB 576 SFRABEKIKHCRVIOEGQSVLSSSEFDSLVDLISYERKHPYRKMKLRYPINEETLEKI 635
OY 122 ARSRQSGVILROEAEV-----VRALDFENGDEEDLPKRGDILIRIRKP 168
DB 636 GTDPDPGALYEGRNPGFYVEANPMTFKGSYRALFDYKAQREDELTFTKNTIIQNVKQ 695
OY 169 EEDWMAAEDSEGRGM-IVPYVEK-YRPA-----SASVALIGC----- 206
DB 696 EGGMMWNG-DCGKKQKQWFPANYVEELFSPAEPERQINDENSPGLDGLGVADVPSCHI 754
OY 207 --NQESHPDP-----LGGPEPGYAPQSVNTPLPNLONGPIYARIYOKRVPA----- 253
DB 755 ARQDVHNGRPFYFTITGLQNLNRYPLDVADVLDEMDQ---WIKIRKRAQYADARLLEG 811
OY 254 ---YDKTALALEVELV 267
      : :|||: |||

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DB 812 KIMERKKIALEISELV 828
RESULT 7
OYIHUT7 PRELIMINARY; PRT: 1010 AA.
ID OYIHUT7
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PHOSPHOLIPASE C-GAMMA-1A (FRAGMENT).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kung H.-F., Kim J., Huang Y.K., Lin M.C.;
RT "Molecular cloning of two different forms of Xenopus phospholipase C-
gamma-1."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF090111; AAD03594.1; -.
DR HSSP; P08487; 2PLD.
DR InterPro; IPR000008; -.
DR InterPro; IPR000909; -.
DR InterPro; IPR000980; -.
DR InterPro; IPR001192; -.
DR InterPro; IPR001452; -.
DR InterPro; IPR001711; -.
DR InterPro; IPR001720; -.
DR InterPro; IPR001849; -.
DR Pfam; PF000017; SH2; 2.
DR Pfam; PF000018; SH3; 1.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00169; PH; 2.
DR Pfam; PF00387; PI-PLC-Y; 1.
DR Pfam; PF00388; PI-PLC-X; 1.
DR PRINTS; PR00390; PHPLIPASEC.
DR PRINTS; PR00678; PI3KINASEP85.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50001; SH2; 2.
DR PROSITE; PS50002; SH3; 1.
DR SMART; SM00252; SH2; 1.
FT NON_TER 1
FT NON_TER 1010
SQ SEQUENCE 1010 AA; 116693 MW; 213247F73EE3EEDA CRC64;

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Query Match      10.6%; Score 184.5; DB 13; Length 1010;
Best Local Similarity 22.5%; Pred. No. 8.5e-07;
Matches 84; Conservative 28; Mismatches 101; Indels 161; Gaps 14;

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```

OY 3 GCAGNFDESER-----SSWYWGRL-----SRQEAVALL-----OGQRHGVL 39
DB 318 GNOANDDEEOKASNSSELSAEMKWFHGLGAGRDGRHIAERLLTDYCIETGADGGSFL 377
OY 40 VRDSTSPGQVYLSVSENSRSHYIINS-----SGPR-----KIHYDITTLIEPV 71
DB 378 VRSETFVGDTYLSFWKNGKVQHCRIHSROEAGSPKFLTDNLVESLYALTLTHQOMPL 437
OY 72 -----PPVPSPAQ-----PPGVSPSRLR----- 91
DB 438 RCNEFEMRLTEPVQTNHAESKEWYHASLTRQAEHMLKRVPRDGAFLVRRKSEQNSYAI 497
OY 92 -----IGDQFDSLPALLEY-----KIHYDITTLIEPV 121
DB 498 SFRABEKIKHCRVIOEGQSVLSSSEFDSLVDLISYERKHPYRKMKLRYPINEETLEKI 557
      : :|||: |||

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RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO EF-HAND FAMILY.
 DR EMBL: AF032118; AAC73068.1; -.
 DR HSSP: P29355; ISEM.
 DR InterPro: IPR000261; -.
 DR InterPro: IPR001452; -.
 DR InterPro: IPR002048; -.
 DR Pfam: PF00018; SH3; 5.
 DR Pfam: PF00036; ehand; 2.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_2.
 DR PROSITE: PS50002; SH3; 5.
 DR SMART: SM00027; EH; 1.
 DR Calcium-binding.
 KW SEQUENCE 1270 AA; 143670 MW; EA940C1F6B6A6858 CRC64;

Query Match 9.5%; Score 165; DB 13; Length 1270;
 Best Local Similarity 24.5%; Pred. No. 4.7e-05;
 Matches 75; Conservative 38; Mismatches 79; Indels 114; Gaps 18;

OY 11 EERSWYGRSLRQEAVALLOGRHGVFLVNDSTSPGDYVLSVSENSRYSHYIINSGP 70
 DB EQQDMWMTGE-----VQGK-GWF-----PKSYKILSGPLRKSTIDTSSE 969
 OY 71 RPYPPSPAPQPPGVSPSLRLRIGQEDFSLPALLEFYKIHLYDTTLIEPVARSQSGV 130
 DB 970 SP-----ASLRVSSPAFK--PAI-----QGE-- 989
 OY 131 ILRQEAIVYALDFENGNDEEDLPFKKGLIRLRDKEQWMAEDSEGRKMTIPVYV 190
 DB 990 -----EYI-SMTYESNEGDLTFQGGDLI-VVIRKDGDMWTGTGE-KTGVFPSTNYV 1039
 OY 191 EKYRPASASVALIGNQSGSHPOPLGPEPGPYAQPSTVPLPNIQNGPIYARVIOKRV 250
 DB 1040 ---RKDEAAG--SGGKTGS-----LKKKEIAQVIA--- 1067
 OY 251 PNAIDKTA---LALVEGLVYKTVINSGWEGF--CNGKR--GHPFTHVRL---D 298
 DB 1068 --SYAATPEQLTLAPGOLLIRKKNPQGWEGELQARQKROIGWPPANVYKLLSPGTN 1125
 OY 299 QONPDE 304
 DB 1126 KSTPTE 1131

RESULT 13
 ID O35413 PRELIMINARY; PRT; 1196 AA.
 AC O35413:
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE SH3-CONTAINING PROTEIN P4015.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN
 RP SEQUENCE FROM N.A.
 RA Ide N., Takeuchi M., Hata Y., Takai Y.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF026505; AAB81527.1; -.
 DR HSSP: P29354; IGRI.
 DR InterPro: IPR000822; -.
 DR InterPro: IPR001452; -.
 DR InterPro: IPR003127; -.
 DR Pfam: PF00018; SH3; 3.
 DR Pfam: PF02208; Sorb; 1.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRODOM: PD016158; -; 1.
 DR PROSITE: PS50002; SH3; 3.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2; UNKNOWN_1.

DR SMART: SM00326; SH3; 1.
 SQ SEQUENCE 1196 AA; 134052 MW; 84E81DFD604D4884 CRC64;

Query Match 9.5%; Score 164; DB 11; Length 1196;
 Best Local Similarity 29.1%; Pred. No. 5.3e-05;
 Matches 57; Conservative 31; Mismatches 70; Indels 38; Gaps 10;

OY 115 TLIEPVARSQSGVITLQEAIEYVRALFPNGNDEEDLPFKKGLIRLRDKEQWMA 174
 DB 942 TDGRSVSRERKGT---EKEVKLPKAYDFKAQTSKELSKGDTVYLIRKIDQWYE 998
 OY 175 AEDSEGRKGMIPVYVEKYRPPASASVALIGNQSGSHPOPLGPEPGPYAQPSTVPLP 234
 DB 999 GE-HHGRVGIFPISYEKLT-----PEK--AQPA--RPP 1029
 OY 235 NIQNGPIYARVIOKRVNAYDKTALALEVGLVYKTVINSGW--EGECNG--KRHFPF 291
 DB 1030 PYQPGEL-GEALAKYFNADTNVELSLRKGRIRILK-RVDQNWYEGRKIPGTNRQIFPV 1087
 OY 292 THYRLIDQNP--DEDF 306
 DB 1088 SYEVYKRNFKGSEDI 1103

RESULT 14
 ID O9P7E8 PRELIMINARY; PRT; 857 AA.
 AC O9P7E8:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE ACTIN BINDING PROTEIN WITH SH3 DOMAINS.
 GN SPABJ760.02C.
 OS Schizosaccharomyces pombe (Fission yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OX NCBI_TaxID=4896;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=972H-;
 RA Harris D., Wood V., Rajandream M.A., Barrell B.G.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL162631; CAB83085.1; -.
 DR InterPro: IPR000108; -.
 DR InterPro: IPR001452; -.
 DR InterPro: IPR002108; -.
 DR InterPro: IPR002965; -.
 DR Pfam: PF00018; SH3; 2.
 DR Pfam: PF00241; cofilin_ADF; 1.
 DR PRINTS: PR00499; P67PHOX.
 DR PRINTS: PR01217; PRICHEXTENS.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PROSITE: PS50002; SH3; 2.
 DR SMART: SM00102; ADF; 1.
 SQ SEQUENCE 857 AA; 91137 MW; 247EFA78BAFE7097 CRC64;

Query Match 9.4%; Score 163.5; DB 3; Length 857;
 Best Local Similarity 23.8%; Pred. No. 3.7e-05;
 Matches 57; Conservative 35; Mismatches 87; Indels 61; Gaps 9;

OY 68 SGPRP-----VPPSPAPQPPGVSPSLRLRIGQEDFSLPALLEFYKIHLYDTTLIEPVAR 123
 DB 663 SVQPPAPAPVVEPSVQPPAVPVVPAAGQLNEPVVPLPPH-----DETQ--EP--- 711
 OY 124 SRQSGVILRQEAIEYVR---ALPDFNGNDEEDLPFKKGLIRLRDKEQWMAEDSE 179
 DB 712 --QVGGDVAKATHQPTPTPAIVITDYSPREENETELVENQIQILFVDDGMMWLGNSK 769
 OY 180 GKGGMIPVYVEKYRPPASASVALIGNQSGSHPOPLGPEPGPYAQPSTVPLPNIQNG 239
 DB 1126 KSTPTE 1131

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Db 770 GGGGFPNSNYE-----ITGNETANNPP-----AEPQAGGP----- 801
Qy 240 PIYARVIOKRPNAYDKTA-----LAEVGLVAVTKINSGWGESECNKRCHGFFPTH 254
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 802 -----GKSKYKALYDQAQEDNQLSFEDELIANVDCVDPNMWEGSGCHGRGFPSNY 854

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RESULT 15

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|----|--|--------------|------|---------|
| TD | 09Y338; | PRELIMINARY; | PRT; | 684 AA. |
| AC | 09Y338; | | | |
| DT | 01-NOV-1999 (TrEMBLrel. 12, Created) | | | |
| DT | 01-MAR-1999 (TrEMBLrel. 12, last sequence update) | | | |
| DT | 01-MAR-2001 (TrEMBLrel. 16, last annotation update) | | | |
| DE | SHP12 PROTEIN. | | | |
| OS | Homo sapiens (human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=LIVER; | | | |
| RA | Liu W.S., Chuang L.M.; | | | |
| RL | Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases. | | | |
| DR | EMBL; AF136380; AAD27647.1; -. | | | |
| DR | HSSP; Q60631; IGBO. | | | |
| DR | InterPro; IPR000108; -. | | | |
| DR | InterPro; IPR001452; -. | | | |
| DR | InterPro; IPR003127; -. | | | |
| DR | Pfam; PF000018; SH3; 3. | | | |
| DR | Pfam; PF02208; Sord; 1. | | | |
| DR | PRINTS; PR00499; P67PHOX. | | | |
| DR | PRINTS; PR00452; SH3DOMAIN. | | | |
| DR | PROSITE; PS50002; SH3; 3. | | | |
| DR | SMART; SM00326; SH3; 1. | | | |
| SQ | SEQUENCE 684 AA; 76341 MW; 2274E632BB07329C CRC64; | | | |

| | | | | | | | |
|-----------------------|-------|--------------|-------|------------|-----|--------|-----|
| Query Match | 9.48 | Score | 163 | DB | 4 | Length | 684 |
| Best Local Similarity | 25.08 | Pred. No. | 3e-05 | | | | |
| Matches | 67 | Conservative | 40 | Mismatches | 103 | Indels | 58 |
| | | | | | | Gaps | 12 |

[illegible]

Search completed: September 27, 2001, 16:43:10
Job time: 178 sec